98 90 90 90	126 179 128 180	216 269 218 270	305 359 307 359	395 449 449
90 KGSYGVDEMDVKSLR KGSHGVDGMKVDELL QGAPGIDGVSTDQLR KGAPGADGMTVADLA	166 180 RRGHNAVRQAKQWMK RSAKQAIKKAKEYWE RNAHDAVRQAQGYIQ RSTHQAIEMARAHVT	270 LDELDNELEKRGLKF LTELDRELEKRGHKF LDDLDKELEKRGLKF LDELDRELERRGHRF	360 KQRIRELTSRRHSMK KAKIKAITARSNALN KQRIRQLTNPNWSIS RDRLRMLLRSVRARK	436 GYWRVAHSPIMDYAL SYWRIANSPILSTTL GAWRTTKTPQLHQAL GPWWNSGAQHMNYAL
75 7 SRENLIGALERVEKN K DRONMLAYKRVKSN K ARDNLITALKRVEAN Q APANLRRAYORVVSN K	151 YDPTFSERSFGFRPH FEKTFSENSYGFRPK FDPDFSPSSFGFRPG FDPLFSDYSYGFRPG	241 PPGGPLSPLLSNIV CPQGGPLSPLLSNIM TPQGGPLSPLLANIL TPQGGPLSPLLSNIL IV	331 -DPKMRVSKESVKRL K -CRIGIRVHEKSVKKF K -KARIRLAPRSIORL K -OPRLRVARMSLDRL R	421 GIKKAKAWQWANSRK GINNSKAWEFANTRK GLKETAVWEIANTRK GLSEERANKSAFNGR
46MLERIL DDGKLYETNLLERILMALLERIL TWTNAEPDTLMERVL	150 EGSYFPKPVRRVEIP KPNGGVRKLGIPTVM DRELQQAIAQILTQL NGKYCFKAVRRVEIP KPNGGVRLGIPTVW DRELQQAIAQILTQL AGTYRPAPVRRVGIP KPGGGTRQLGIPTVV DRLIQQAILQELTPI AGEYHPQAV <u>RAVEIP K</u> PQGGT <u>RQLGIPTVV DR</u> LIQQALQQQLTPI I	226 TGVMERGLVSPNTEG SGWINGVVSETERG AGVMIEGVKVQTEFG AGIMSGGVVSPROEG	330 PWNRKFLGFSFTRGK PWRRKFLGFTFYOWY PWKRAFLGFSFTPER AWKCDYLGYGMSWHQ	405 406 420  RWK EWKTTSARQKNLVRL  YWK QWKKVKTKYDNLRKF  QWL QWKRVRTRIRELRAL  IWR QWKQPPTRLRNLMRL
31 45  STRAHSISTAFDRRK  PRVMPDSAKVPAASA	121 135 KPNGGVRKLGIPTWM KPDGGIRLLGIPTWW KPGGGTRQLGIPTWV KPGGGTRQLGIPTWV I I I I I I I I I I I I I I I I I I I	211 1QDPRVLQLIRRYLQ IKDKRVLKLIRLYLQ VKDKRVLKLIRAYLQ IKDKCVLRLIRRYLE	301 RLKLKVNREKSAVDR KLKLKVNREESAVDR TLKLKVNEEKSAVDR RLKLTVNRRKSQVAR VI	391 IDAWIRRLEMI LDEWTRRLEMC LDEWIRRLERC LDGWVRHKLRCV
16 30  YKEGWSCEIRVELQN 	106 120 EGSYFPKPVRRVEIP NGKYCPKAVRRVEIP AGTYRPAPVRRVGIP AGEYHPQAVRAVEIP	210 DKVNHDRLMRKLSSR DTVNHDKLMALVARK DRVNHDILMSRVARK DRVNHDILMACIERR	286 AGIRIMESVTSFIEN AGDRVMRSITRFIEN AGQRVKQSIQRFLEK AGERVLVSVER <u>FIRE</u>	YY 376 390 LGYYQVVDTPSILAQ LNYFGIAEMTKLAKK IGYFKLVETPSVLQT ASYFKLSQSKRPLEE
1 	105 LHLHENWTSIRNEII QYLKQNGKTLIASIF DYIRAHWSTIRAQLL GYVKQYWPTLKARLL	181 EGYRWVVDIDLEKFF EGYKWVVDIDLAKYF EGYRYVVDMDLEKFF AGHRWCVELDLEKFF	271 285 VRYADDCNIYVRSKR CRYADDNNVYVRSKK CRYADDCNIYVKSLR VRYADDANIYVRSPR V	LN G 361 375 MSDRLRRLNRYLIGW IENRIIKLRQCIIGW MPERIHRVNQYVMGW MATVIERINPVLRGW
1 2 C.acetobutylicum -MKN 3 Bst803-2065 9 PalcaligenesMatur MPPV	91 1 B.halodurans LHIH 2 C.acetobutylicum QYLK 3 <b>Bst803-2065</b> DYIK 4 PalcaligenesMatur GYVK	181 195 1 B.halodurans EGYRWVVDIDLEKFF 2 C.acetobutylicum EGYKWVVDIDLEKFF 3 Bst803-2065 EGYRVVDMDLEKFF 4 PalcaligenesMatur AGHRWCVELDLEKFF III	271 285 1 B.halodurans VRYADDCNIYVRSKR 2 C.acetobutylicum CRYADDNNVYVRSKK 3 Bst803-2065 CRYADDCNIYVKSLR 4 PalcaligenesMatur VRYADDANIYVRSPR	361 1 B.halodurans MSDR 2 C.acetobutylicum IENR 3 Bst803-2065 MPER 4 PalcaligenesMatur MATV

Fig. 1

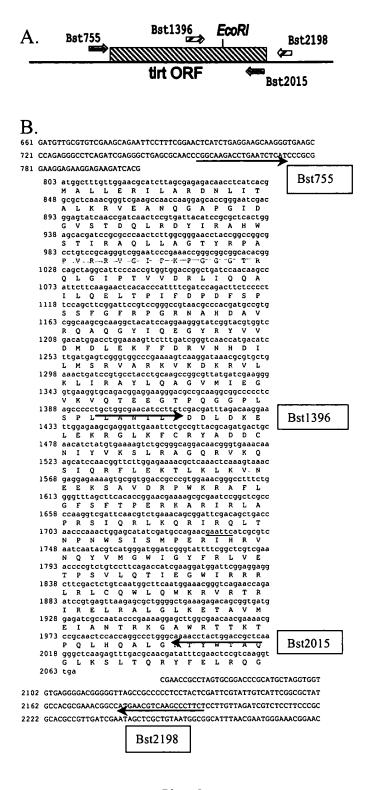


Fig. 2

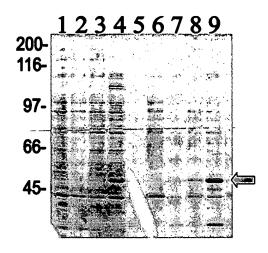


Fig. 3

## S1234567891011121314

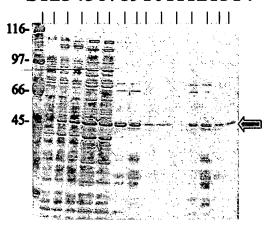


Fig. 4

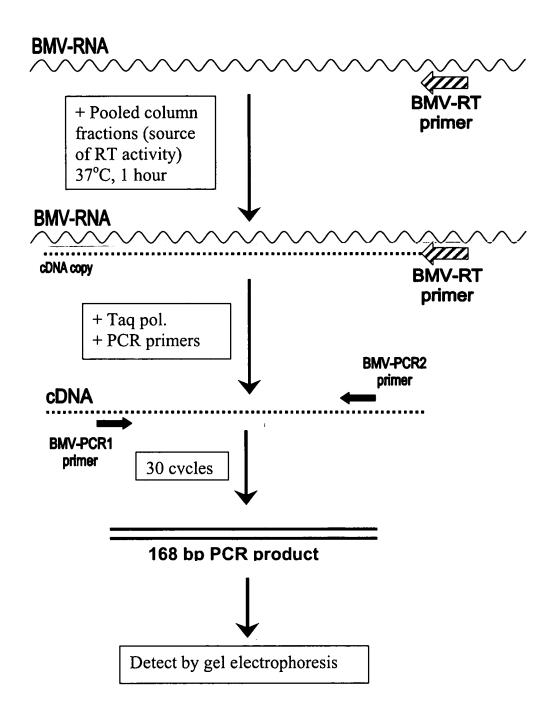


Fig. 5

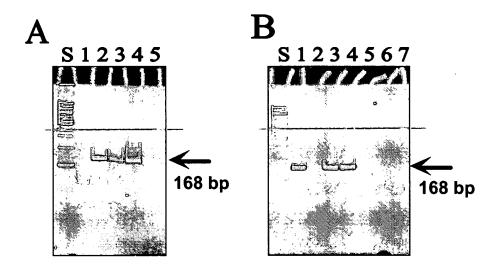


Fig. 6

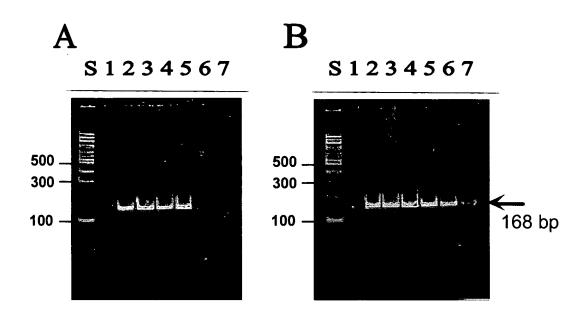
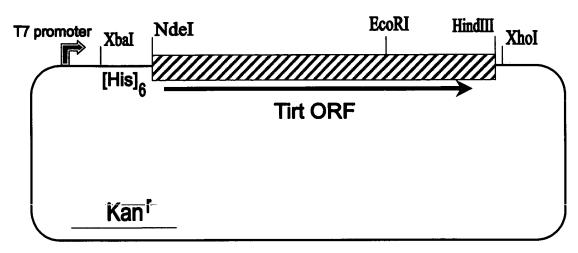


Fig. 7





Plasmid pTirt#16

## Β.

## T7 promoter CNAC TCAC

1 TGGNNNAGT NTTTAAACCT TTGNACCGCC NTAATACNAC TCACTATAGG

| lac operator | | GGAATTGTGA GCGGATAACA ATTCCCCTCT | AGAAATAATT | TTNTTTAACT | TTNTTTAACT | TTNTTTAACT | TTNTTTAACT | TTNTTTAACT | TTNTTTAACT |